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RAW SEQUENCE LISTING   DATE: 11/21/2002
PATENT APPLICATION: US/09/849,868   TIME: 14:37:22

Input Set : A:\US09849868.TXT
Output Set: N:\CRF4\11212002\I849868.raw

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 4 <110> APPLICANT: Gao, Wei-Qiang
 6 <120> TITLE OF INVENTION: HAIR CELL DISORDERS
 9 <130> FILE REFERENCE: GENENT.035C1
11 <140> CURRENT APPLICATION NUMBER: US 09/849,868
12 <141> CURRENT FILING DATE: 2001-05-04
14 <150> PRIOR APPLICATION NUMBER: US 60/107,522
15 <151> PRIOR FILING DATE: 1998-11-07
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/25744
18 <151> PRIOR FILING DATE: 1999-10-28
20 <160> NUMBER OF SEQ ID NOS: 14
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 669
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
30 Ala Arg Ala Pro Gln Arg Gly Arg Ser Leu Ser Pro Ser Arg Asp Lys
31  1               5                  10                  15
32 Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly Pro Asn Ser Pro Ala Pro
33              20                  25                  30
34 Arg Ala Val Arg Val Glu Arg Ser Val Ser Gly Glu Met Ser Glu Arg
35          35                  40                  45
36 Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Glu Arg Gly Ser
37      50                  55                  60
38 Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro
39 65                  70                  75                  80
40 Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys
41              85                  90                  95
42 Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe
43              100                 105                 110
44 Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln
45          115                 120                 125
46 Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn
47      130                 135                 140
48 Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser
49 145                 150                 155                 160
50 Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser
51              165                 170                 175
52 Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val
53              180                 185                 190
54 Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn
55              195                 200                 205
56 Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
```

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```
57    210                    215                    220
58 Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
59 225                    230                    235                    240
60 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
61                    245                    250                    255
62 Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
63                    260                    265                    270
64 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu
65                    275                    280                    285
66 Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys
67    290                    295                    300
68 Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp
69 305                    310                    315                    320
70 Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile
71                    325                    330                    335
72 Ala Asn Gly Pro His His Pro Asn Pro Pro Glu Asn Val Gln Leu
73                    340                    345                    350
74 Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val
75                    355                    360                    365
76 Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr
77    370                    375                    380
78 Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser
79 385                    390                    395                    400
80 Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile Val
81                    405                    410                    415
82 Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro
83                    420                    425                    430
84 Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe
85                    435                    440                    445
86 Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His
87    450                    455                    460
88 Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
89 465                    470                    475                    480
90 Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met
91                    485                    490                    495
92 Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala Val
93                    500                    505                    510
94 Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro
95    515                    520                    525
96 Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser
97    530                    535                    540
98 Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser Pro
99 545                    550                    555                    560
100 Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu
101                    565                    570                    575
102 Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala Lys
103                    580                    585                    590
104 Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser
105    595                    600                    605
```

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```
106 Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu
107     610             615             620
108 Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala
109 625             630             635             640
110 Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg Thr
111             645             650             655
112 Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln
113             660             665
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 2226
118 <212> TYPE: DNA
119 <213> ORGANISM: Homo sapiens
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (2)...(2008)
125 <400> SEQUENCE: 2
126 g ggc gcg agc gcc tca gcg cgg ccg ctc gct ctc ccc ctc gag gga caa 49
127   Gly Ala Ser Ala Ser Ala Arg Pro Leu Ala Leu Pro Leu Glu Gly Gln
128   1           5               10              15
130 act ttt ccc aaa ccc gat ccg agc cct tgg acc aaa ctc gcc tgc gcc 97
131 Thr Phe Pro Lys Pro Asp Pro Ser Pro Trp Thr Lys Leu Ala Cys Ala
132             20              25              30
134 gag agc cgt ccg cgt aga gcg ctc cgt ctc cgg cga gat gtc cga gcg 145
135 Glu Ser Arg Pro Arg Arg Ala Leu Arg Leu Arg Arg Asp Val Arg Ala
136             35              40              45
138 caa aga agg cag agg caa agg gaa ggg caa gaa gaa gga gcg agg ctc 193
139 Gln Arg Arg Gln Arg Gln Arg Glu Gly Gln Glu Glu Gly Ala Arg Leu
140     50              55              60
142 cgg caa gaa gcc gga gtc cgc ggc ggg cag cca gag ccc agc ctt gcc 241
143 Arg Gln Glu Ala Gly Val Arg Gly Gly Gln Pro Glu Pro Ser Leu Ala
144 65              70              75              80
146 tcc ccg att gaa aga gat gaa aag cca gga atc ggc tgc agg ttc caa 289
147 Ser Pro Ile Glu Arg Asp Glu Lys Pro Gly Ile Gly Cys Arg Phe Gln
148             85              90              95
150 act agt cct tcg gtg tga aac cag ttc tga ata ctc ctc tct cag att 337
151 Thr Ser Pro Ser Val  *  Asn Gln Phe  *  Ile Leu Leu Ser Gln Ile
152             100             105             110
154 caa gtg gtt caa gaa tgg gaa tga att gaa tcg aaa aaa caa acc aca 385
155 Gln Val Val Gln Glu Trp Glu  *  Ile Glu Ser Lys Lys Gln Thr Thr
156             115             120             125
158 aaa tat caa gat aca aaa aaa gcc agg gaa gtc aga act tcg cat taa 433
159 Lys Tyr Gln Asp Thr Lys Lys Ala Arg Glu Val Arg Thr Ser His  *
160             130             135             140
162 caa agc atc act ggc tga ttc tgg aga gta tat gtg caa agt gat cag 481
163 Gln Ser Ile Thr Gly  *  Phe Trp Arg Val Tyr Val Gln Ser Asp Gln
164             145             150             155
166 caa att agg aaa tga cag tgc ctc tgc caa tat cac cat cgt gga atc 529
167 Gln Ile Arg Lys  *  Gln Cys Leu Cys Gln Tyr His His Arg Gly Ile
168             160             165             170
```

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```
170 aaa cga gat cat cac tgg tat gcc agc ctc aac tga agg agc ata tgt   577
171 Lys Arg Asp His His Trp Tyr Ala Ser Leu Asn  *  Arg Ser Ile Cys
172             175             180                     185
174 gtc ttc aga gtc tcc cat tag aat atc agt atc cac aga agg agc aaa   625
175 Val Phe Arg Val Ser His  *  Asn Ile Ser Ile His Arg Arg Ser Lys
176             190             195                     200
178 tac ttc ttc atc tac atc tac atc cac cac tgg gac aag cca tct tgt   673
179 Tyr Phe Phe Ile Tyr Ile Tyr Ile His His Trp Asp Lys Pro Ser Cys
180             205             210                     215
182 aaa atg tgc gga gaa gga gaa aac ttt ctg tgt gaa tgg agg gga gtg   721
183 Lys Met Cys Gly Glu Gly Glu Asn Phe Leu Cys Glu Trp Arg Gly Val
184             220             225                     230
186 ctt cat ggt gaa aga cct ttc aaa ccc ctc gag ata ctt gtg caa gtg   769
187 Leu His Gly Glu Arg Pro Phe Lys Pro Leu Glu Ile Leu Val Gln Val
188             235             240                     245
190 cca acc tgg att cac tgg agc aag atg tac tga gaa tgt gcc cat gaa   817
191 Pro Thr Trp Ile His Trp Ser Lys Met Tyr  *  Glu Cys Ala His Glu
192     250             255                     260
194 agt cca aaa cca aga aaa ggc gga gga gct gta cca gaa gag agt gct   865
195 Ser Pro Lys Pro Arg Lys Gly Gly Gly Ala Val Pro Glu Glu Ser Ala
196     265             270                     275
198 gac cat aac cgg cat ctg cat cgc cct cct tgt ggt cgg cat cat gtg   913
199 Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg His His Val
200 280                 285                 290                 295
202 tgt ggt ggc cta ctg caa aac caa gaa aca gcg gaa aaa gct gca tga   961
203 Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys Ala Ala  *
204             300             305                     310
206 ccg tct tcg gca gag cct tcg gtc tga acg aaa caa tat gat gaa cat  1009
207 Pro Ser Ser Ala Glu Pro Ser Val  *  Thr Lys Gln Tyr Asp Glu His
208             315             320                     325
210 tgc caa tgg gcc tca cca tcc taa ccc acc ccc cga gaa tgt cca gct  1057
211 Cys Gln Trp Ala Ser Pro Ser  *  Pro Thr Pro Arg Glu Cys Pro Ala
212             330             335                     340
214 ggt gaa tca ata cgt atc taa aaa cgt cat ctc cag tga gca tat tgt  1105
215 Gly Glu Ser Ile Arg Ile  *  Lys Arg His Leu Gln  *  Ala Tyr Cys
216             345             350
218 tga gag aga agc aga gac atc ctt ttc cac cag tca cta tac ttc cac  1153
219  *  Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu Tyr Phe His
220     355             360                     365
222 agc cca tca ctc cac tac tgt cac cca gac tcc tag cca cag ctg gag  1201
223 Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser  *  Pro Gln Leu Glu
224 370             375                     380
226 caa cgg aca cac tga aag cat cct ttc cga aag cca ctc tgt aat cgt  1249
227 Gln Arg Thr His  *  Lys His Pro Phe Arg Lys Pro Leu Cys Asn Arg
228 385                 390                     395
230 gat gtc atc cgt aga aaa cag tag gca cag cag ccc aac tgg ggg ccc  1297
231 Asp Val Ile Arg Arg Lys Gln  *  Ala Gln Gln Pro Asn Trp Gly Pro
232 400             405                     410
234 aag agg acg tct taa tgg cac agg agg ccc tcg tga atg taa cag ctt  1345
```

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```
235 Lys Arg Thr Ser  *  Trp His Arg Arg Pro Ser  *  Met  *  Gln Leu
236 415                     420                 425
238 cct cag gca tgc cag aga aac ccc tga ttc cta ccg aga ctc tcc tca   1393
239 Pro Gln Ala Cys Gln Arg Asn Pro  *  Phe Leu Pro Arg Leu Ser Ser
240         430             435                     440
242 tag tga aag gta tgt gtc agc cat gac cac ccc ggc tcg tat gtc acc   1441
243  *   *  Lys Val Cys Val Ser His Asp His Pro Gly Ser Tyr Val Thr
244             445             450                     455
246 tgt aga ttt cca cac gcc aag ctc ccc caa atc gcc ccc ttc gga aat   1489
247 Cys Arg Phe Pro His Ala Lys Leu Pro Gln Ile Ala Pro Phe Gly Asn
248         460             465                     470
250 gtc tcc acc cgt gtc cag cat gac ggt gtc cat gcc ttc cat ggc ggt   1537
251 Val Ser Thr Arg Val Gln His Asp Gly Val His Ala Phe His Gly Gly
252         475             480                     485
254 cag ccc ctt cat gga aga aga gag acc tct act tct cgt gac acc acc   1585
255 Gln Pro Leu His Gly Arg Arg Glu Thr Ser Thr Ser Arg Asp Thr Thr
256     490             495                 500
258 aag gct gcg gga gaa gaa gtt tga cca tca ccc tca gca gtt cag ctc   1633
259 Lys Ala Ala Gly Glu Glu Val  *  Pro Ser Pro Ser Ala Val Gln Leu
260 505             510                 515
262 ctt cca cca caa ccc cgc gca tga cag taa cag cct ccc tgc tag ccc   1681
263 Leu Pro Pro Gln Pro Arg Ala  *  Gln  *  Gln Pro Pro Cys  *  Pro
264 520             525                 530
266 ctt gag gat agt gga gga tga gga gta tga aac gac cca aga gta cga   1729
267 Leu Glu Asp Ser Gly Gly  *  Gly Val  *  Asn Asp Pro Arg Val Arg
268         535             540                 545
270 gcc agc cca aga gcc tgt taa gaa act cgc caa tag ccg gcg ggc caa   1777
271 Ala Ser Pro Arg Ala Cys  *  Glu Thr Arg Gln  *  Pro Ala Gly Gln
272         550                     555                 560
274 aag aac caa gcc caa tgg cca cat tgc taa cag att gga agt gga cag   1825
275 Lys Asn Gln Ala Gln Trp Pro His Cys  *  Gln Ile Gly Ser Gly Gln
276         565                     570                 575
278 caa cac aag ctc cca gag cag taa ctc aga gag tga aac aga aga tga   1873
279 Gln His Lys Leu Pro Glu Gln  *  Leu Arg Glu  *  Asn Arg Arg  *
280         580                     585
282 aag agt agg tga aga tac gcc ttt cct ggg cat aca gaa ccc cct ggc   1921
283 Lys Ser Arg  *  Arg Tyr Ala Phe Pro Gly His Thr Glu Pro Pro Gly
284     590                 595                 600
286 agc cag tct tga ggc aac acc tgc ctt ccg cct ggc tga cag cag gac   1969
287 Ser Gln Ser  *  Gly Asn Thr Cys Leu Pro Pro Gly  *  Gln Gln Asp
288     605                 610                 615
290 taa ccc agc agg ccg ctt ctc gac aca gga aga aat cca ggccaggctg   2018
291  *  Pro Ser Arg Pro Leu Leu Asp Thr Gly Arg Asn Pro
292         620             625
294 tctagtgtaa ttgctaacca agaccctatt gctgtataaa acctaaataa acacatagat 2078
295 tcacctgtaa aactttattt tatataataa agtattccac cttaaattaa acaatttatt 2138
296 ttattttagc agttctgcaa atagaaaaca ggaaaaaaac ttttataaat taaatatatg 2198
297 tatgtaaaaa tgaaaaaaaa aaaaaaa                                      2226
299 <210> SEQ ID NO: 3
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VERIFICATION SUMMARY
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